

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/583,127  
Source: IFW/O  
Date Processed by STIC: 7/27/06

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 07/27/2006

PATENT APPLICATION: US/10/583,127

TIME: 10:27:25

Input Set : A:\FS04-421PCT sequence list.ST25.txt

Output Set: N:\CRF4\07272006\J583127.raw

3 <110> APPLICANT: Two Cells. Co. Ltd  
 5 <120> TITLE OF INVENTION: Bactericide against Streptococcus mutans and Streptococcus  
 sobrinus  
 7 <130> FILE REFERENCE: PFS04-421PCT  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/583,127  
 C--> 9 <141> CURRENT FILING DATE: 2006-06-16  
 9 <160> NUMBER OF SEQ ID NOS: 4  
 11 <170> SOFTWARE: PatentIn version 3.1  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 979  
 15 <212> TYPE: PRT  
 16 <213> ORGANISM: Streptococcus mutans  
 18 <400> SEQUENCE: 1  
 20 Met Lys Ser Lys Thr Tyr Leu Met Ile Pro Leu Ala Leu Thr Leu Phe  
 21 1 5 10 15  
 24 Met Ala Ala Asn Lys Ile Ser Ala Asp Glu Gln Asn Gln Ser Leu Ser  
 25 20 25 30  
 28 Ala Ser Glu Val Ile Ser Ser Asp Ala Thr Ser Val Ser Glu Leu Pro  
 29 35 40 45  
 32 Ala Thr Thr Ala Gln Ile Ser Gln Glu Val Arg Asn Asn Gly Gln Asp  
 33 50 55 60  
 36 Ser Thr Ile Gln Leu Gln Thr Gln Glu Gln Ser Asp Pro Ile Thr  
 37 65 70 75 80  
 40 Ser Thr Ser Glu Thr Thr Val Ser Ser Met Lys Ala Val Thr Asn Gly  
 41 85 90 95  
 44 Ser Pro Ala Lys Ala Asn Glu Thr Glu Thr Val Pro Ser Gln Ala Ser  
 45 100 105 110  
 48 Thr Ala Ser Ser Val Gln Thr Pro Asp Gln Ile Ser Thr Val Pro Ser  
 49 115 120 125  
 52 Val Lys Ala Glu Thr Thr Ser Thr Ala Asp Gln Leu Gln Ser Thr Ser  
 53 130 135 140  
 56 Ser Ala Pro Leu Asp Gln Gln Thr Asp Ala Lys Arg Leu Ser Asn Lys  
 57 145 150 155 160  
 60 Met Thr Pro Ala Ser Ser Val Gln Ala Arg Ser Ser Leu Thr Gln Asp  
 61 165 170 175  
 64 Lys Gln Val Gln Ala Gln Glu Val Thr Ser Ala Val Val Glu Glu Lys  
 65 180 185 190  
 68 Gly Ile Lys Leu Gln Tyr Asn Gly Gln Ile Ala Arg Asn Thr Lys Ile  
 69 195 200 205  
 72 Gln Phe Ala Val Trp Ser Ala Arg Asn Asp Gln Asp Asp Leu Gln Trp  
 73 210 215 220  
 76 Tyr Thr Ala Asn Asn Met Gly Ala Ala Tyr Ala Glu Phe Lys Asn His  
 77 225 230 235 240  
 80 Arg Glu Tyr Gly Thr Tyr Tyr Val His Thr Tyr Ala Asn Gln Asn Gly

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```

81          245          250          255
84 Lys Met Ile Gly Leu Asn Ala Thr Thr Leu Thr Ile Ala Gln Pro Gln
85          260          265          270
88 Val Gln Thr Asn Ile Gln Arg Lys Ser Ala Thr Asn Phe Glu Leu Thr
89          275          280          285
92 Val Ser Asn Val Pro Asn Thr Ile Ser Ser Ile Met Val Pro Val Trp
93 290          295          300
96 Ser Asp Gln Asn Gly Gln Asp Asp Ile Lys Trp Tyr Asn Ala Arg Lys
97 305          310          315          320
100 Ala Asp Asp Gly Ser Tyr Lys Ala Leu Ile Asp Thr Lys Asn His Lys
101          325          330          335
104 Asn Asp Leu Gly His Tyr Glu Ala His Ile Tyr Gly Tyr Ser Thr Val
105          340          345          350
108 Thr Gln Ser Gln Ile Gly Leu Ala Val Ser Ser Gly Phe Asp Arg Asn
109          355          360          365
112 Asp Thr Arg Pro Asn Ala Arg Ile Ser Val Ala Asp Tyr Asp Gln Asn
113          370          375          380
116 Lys Thr Thr Phe Asp Val Val Val Glu Gly Ser Ser Asp Thr Lys Thr
117 385          390          395          400
120 Val Ser Ala Val Asn Ile Ala Val Trp Ser Glu Asp Lys Gly Gln Asp
121          405          410          415
124 Asp Leu Lys Trp Tyr Ser Pro Lys Ile Val Asn Asn Lys Ala Thr Val
125          420          425          430
128 Thr Ile Asn Ile Ala Asn His Ser Asn Thr Ser Asp Lys Tyr Asn Val
129          435          440          445
132 His Val Tyr Thr Asp Tyr Thr Asp Gly Thr His Ser Gly Thr Ile Leu
133          450          455          460
136 Gly Ala Tyr Gln Ile Asn Lys Pro Leu Glu Lys Asn Thr Val Ser Ala
137 465          470          475          480
140 Asp Leu Thr Ser Asp Gly Ile Ala Leu Lys Leu Asp Ser Asn Thr Val
141          485          490          495
144 Thr Asp Tyr Thr Lys Val Arg Phe Ala Val Trp Ser Asp Gln Asn Gly
145          500          505          510
148 Gln Asp Asp Leu Lys Trp Tyr Ser Ala Asn Ser Asp Gly Ala Ala Thr
149          515          520          525
152 Ala Ala Tyr Ser Asn His Ser Gly Tyr Gly Leu Tyr His Ile His Thr
153          530          535          540
156 Tyr Ile Ile Lys Asp Gly Glu Met Val Gly Leu Asn Gly Arg Thr Ile
157 545          550          555          560
160 Thr Ile Asn Gln Pro Ser Ala Lys Val Asp Ile Ala Lys Glu Ser Asp
161          565          570          575
164 Ala Leu Tyr Lys Val Thr Val Ser Asn Leu Pro Ala Tyr Ile Ser Ser
165          580          585          590
168 Val Ala Ile Pro Val Trp Thr Asp Lys Asn Asn Gln Asp Asp Ile Gln
169          595          600          605
172 Trp Ile Leu Ala Thr Lys Gln Gly Asp Gly Thr Tyr Ala Ala Gln Ile
173          610          615          620
176 Gln Leu Ala Asp His Asn Gly Glu Thr Gly His Tyr Asn Val His Val
177 625          630          635          640

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180 Tyr Gly Gln Ser Lys Phe Asp Asn Lys Thr Val Gly Leu Ala Ala Thr
181          645          650          655
184 Asp Gly Phe Asn Val Ala Glu Thr Arg Asn Ala Val Ile Ala Ala Ser
185          660          665          670
188 Asn Tyr Asn Ala Ser Ala Gly Thr Ile Asp Met Ile Val Lys Gln Glu
189          675          680          685
192 Ala Gly Gly Lys Ala Ile Lys Glu Val Arg Ile Ala Ala Trp Ser Glu
193          690          695          700
196 Ala Asp Gln Ser Asn Leu His Trp Tyr Val Ser Ser Thr Ile Ile Asp
197 705          710          715          720
200 Gly Lys Val Thr Val Thr Ile Asn Glu Lys Asn His Gln Tyr Ile Lys
201          725          730          735
204 Gly Asn Tyr Asn Ile His Val Tyr Val Asp Tyr Thr Asp Gly Thr Ser
205          740          745          750
208 Ser Gly Thr Asn Ile Gly Asn Tyr Ser Leu Asn Ala Asp Lys Pro Ala
209          755          760          765
212 Val Ala Leu Pro Ser Tyr Phe Ile Asp Ile Ser Ser His Asn Gly Ile
213          770          775          780
216 Ile Ser Val Ala Glu Phe Asn Ser Leu Lys Gln Gln Gly Ile Gln Gly
217 785          790          795          800
220 Val Val Val Lys Leu Thr Glu Gly Thr Ser Tyr Ile Asn Pro Tyr Ala
221          805          810          815
224 Ser Ser Gln Ile Ala Asn Ala Arg Ala Ala Gly Ile Lys Val Ser Ala
225          820          825          830
228 Tyr His Tyr Ala His Tyr Thr Ser Ala Ala Gly Ala Gln Glu Glu Ala
229          835          840          845
232 Arg Tyr Phe Ala Asn Ala Ala Arg Ser Phe Gly Leu Glu Ala Ser Thr
233          850          855          860
236 Val Met Val Asn Asp Met Glu Glu Ser Ser Met Val Asn Asn Ile Asn
237 865          870          875          880
240 Asn Asn Val Gln Ala Trp Gln Asp Glu Met Arg Arg Gln Gly Tyr Ser
241          885          890          895
244 Asn Leu Ile His Tyr Thr Met Ala Ser Trp Leu Asp Ile Arg Gly Gly
245          900          905          910
248 Gln Val Asp Thr Ala Arg Phe Gly Ile Asn Asn Phe Trp Val Ala His
249          915          920          925
252 Tyr Ala Lys Gly Tyr Thr Tyr Met Thr Gln Glu Glu Ala Lys Ser Leu
253          930          935          940
256 Asn Tyr Tyr Ala Asn Ala Ala Ala Trp Gln Tyr Thr Ser Val Ser Ser
257 945          950          955          960
260 Lys Leu Ser His Ala Leu Asp Glu Asn Ile Asp Tyr Thr Gly Arg Phe
261          965          970          975
264 Thr Gln Gln
268 <210> SEQ ID NO: 2
269 <211> LENGTH: 2940
270 <212> TYPE: DNA
271 <213> ORGANISM: Streptococcus mutans
273 <400> SEQUENCE: 2
274 atgaaaagca aaacttattt gatgattcca ttagcattga ccctatttat ggctgcta

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```

276 aaaatatctg cagatgagca aaatcaatcc ttaagtgcac cagaagttat ttcttctgat 120
278 gcgacatcag tatctgaatt accagcgaca acagcacaga taagtcagga agtcagaaat 180
280 aatggacaag acagtactat tcaattgcag caaacacagg aacagtctga tccgataaca 240
282 agtacgtctg agacaactgt ttctctctatg aaggcgggtca caaatggctc acctgccaaa 300
284 gcaaattgaga ctgaaacagt tccgtctcag gcaagtactg ctagtctctgt gcagactcct 360
286 gatcagattt cgactgttcc ctctgtaaaa gcagaaacca cttctaccgc agatcaatta 420
288 caatcaacat catctgctcc tttggatcaa caaactgatg ctaaacgtct ttccaataaa 480
290 atgactccag caagcagcgt acaagctcgt tcttctctta cacaagacaa gcaagtacag 540
292 gcacaggaag tcacaagtgc tgtagtggaa gaaaaagggg ttaagctaca gtataacggt 600
294 cagatcgctc gaaataactaa gattcaattt gctgtctggt cagctcgaaa tgatcaagat 660
296 gatcttcaat ggtatacggc aaataatatg ggagcggcct atgctgaatt caagaatcat 720
298 cgtgagtatg ggacctatta tgttcatact tatgctaate aaaatggcaa gatgatagga 780
300 cttaacgcaa caactcttac aattgctcaa cctcaggtgc aaactaatat tcaaagaaaa 840
302 tcagcaacga attttgagtt aaccgtttct aatgttctta atactattag cagcatcatg 900
304 gtacctgtct ggtcagatca aaacgggtcaa gatgatatta aatgggtataa tgcccgaag 960
306 gctgatgatg gcagttataa ggctttgatt gatactaaaa atcacaagaa tgatttggga 1020
308 cattatgaag ctcatattta cggctacagc acagtaaccc agtctcaaat tggcttagct 1080
310 gttagtctct gttttgaccg caatgatact agaccaatg caaggatatac tgttgctgat 1140
312 tatgacaaaa ataaaacgac ctttgatggt gttgttgagg gttcatctga taaaagact 1200
314 gtatctgctg ttaatatggc tgtttggtct gaagataaag gtcaagatga ccttaagtgg 1260
316 tattcaccaa aaattgtcaa caataaggca actgtgacga ttaatatcgc taatcattca 1320
318 aatacttcag ataaatataa tgtccatggt tatacagact aactgatgg gacacattct 1380
320 ggtactatct taggggctta tcagatcaat aaaccgcttg agaaaaatac tgtttcagct 1440
322 gatttaacta gtgatggcat tgctctcaaa ttagattcaa acacgggtac agattatacc 1500
324 aaagtacgat ttgccgtttg gtcggatcaa aatggtcaag atgatctcaa gtggtatagt 1560
326 gcaaattagt atggagcggc aactgcagct tacagtaacc acagtgggta tgggctttat 1620
328 catatccata cttatattat taaagatggg gaaatgggtg ggcttaattg cagaacgata 1680
330 actattaata agcctagtgc caagggtgat attgctaaag aatccgatgc tctttataaa 1740
332 gtgactgttt ctaacctgcc agcttacatt agttcagtag ctattcctgt ctggacagat 1800
334 aaaaacaatc aagatgatat tcaatggatt ctgcgcacaa aacaagggtg tgggaacctac 1860
336 gcagcgcaaa ttcagttagc tgatcataat ggggaaacag gccattataa tgttcatgtc 1920
338 tatggacaaa gtaaatattg caataaaacg gttggcttag cagcaactga tggctttaat 1980
340 gttgcagaga caaggaatgc tgttatcgtc gcttcaaatt ataatgccag tgcaggaacg 2040
342 atagatatga ttgttaaaca agaagcgggt ggtaaagcga tcaaagaagt tccgatagct 2100
344 gcttgggtcag aagctgatca atctaaccct cattgggtatg tttcatcaac tattattgat 2160
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348 attcatgtct atgttgatta tactgatggc actagtagcg gaaccaatat tggaaactat 2280
350 agcttgaatg ctgataaacc tgctgttgct ctgccatctt actttattga tattagtagc 2340
352 cacaatggaa tcatttctgt tgccgaattc aatagcttga aacaacaagg tattcaagga 2400
354 gtggttggtt agttaacaga aggtacaagc tacatcaatc cttatgcaag ttctcaaatt 2460
356 gccaatgcca gagctgccgg tattaagggt tctgcttacc actatgctca ctatacttct 2520
358 gcggctgggg cacaagaaga agcccgttat tttgctaatt cagccagatc ctttgggttg 2580
360 gaggcaccaa ctgtcatggt caatgatatg gaagagtcct ctatggtgaa caatattaat 2640
362 aataatgttc aagcttggca agatgagatg aggcgtcaag gttatagcaa cctgattcat 2700
364 tatactatgg ctagtgtgtt ggatatacgc ggtgggcaag tagacactgc aagggttggc 2760
366 atcaataatt tttgggttgc tcattatgcc aaaggggtata cttatatgac tcaagaagaa 2820
368 gctaaatccc ttaattatta tgctaatagc gcagcttggc agtatactag tgtatcgtct 2880
370 aaattgtctc atgctttgga tgaaaatatt gattatactg gtcgatttac tcaacagtaa 2940
373 <210> SEQ ID NO: 3

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Input Set : A:\FS04-421PCT sequence list.ST25.txt

Output Set: N:\CRF4\07272006\J583127.raw

374 <211> LENGTH: 20  
375 <212> TYPE: DNA  
376 <213> ORGANISM: artificial sequence  
378 <220> FEATURE:  
379 <223> OTHER INFORMATION: primer  
381 <400> SEQUENCE: 3  
382 agttcctgcc atactactgt 20  
385 <210> SEQ ID NO: 4  
386 <211> LENGTH: 28  
387 <212> TYPE: DNA  
388 <213> ORGANISM: artificial sequence  
390 <220> FEATURE:  
391 <223> OTHER INFORMATION: primer  
393 <400> SEQUENCE: 4  
394 caggatccgt acaagctcgt tcttctct 28

**VERIFICATION SUMMARY**

DATE: 07/27/2006

PATENT APPLICATION: US/10/583,127

TIME: 10:27:26

Input Set : A:\FS04-421PCT sequence list.ST25.txt

Output Set: N:\CRF4\07272006\J583127.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date